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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/086,542A

DATE: 08/09/2002  
TIME: 15:49:57

Input Set : N:\Crf3\RULE60\10086542A.RAW  
Output Set: N:\CRF4\08092002\J086542A.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Wahl, Geoffrey M

6 O'Gorman, Stephen V

8 (ii) TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN

9 MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL  
10 THEREFOR

12 (iii) NUMBER OF SEQUENCES: 4

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Pretty, Schroeder, Brueggemann &amp; Clark

16 (B) STREET: 444 South Flower Street, Suite 2000

17 (C) CITY: Los Angeles

18 (D) STATE: California

19 (E) COUNTRY: USA

20 (F) ZIP: 90071

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

28 (vi) CURRENT APPLICATION DATA:

C--&gt; 29 (A) APPLICATION NUMBER: US/10/086,542A

C--&gt; 30 (B) FILING DATE: 28-Feb-2002

31 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US/08/484,324

36 (B) FILING DATE: 07-JUN-1995

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Reiter, Stephen E

41 (B) REGISTRATION NUMBER: 31,192

42 (C) REFERENCE/DOCKET NUMBER: P41 9984

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: (619) 546-4737

46 (B) TELEFAX: (619) 546-9392

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 1380 base pairs

53 (B) TYPE: nucleic acid

54 (C) STRANDEDNESS: single

55 (D) TOPOLOGY: linear

57 (ii) MOLECULE TYPE: DNA (genomic)

60 (vii) IMMEDIATE SOURCE:

61 (B) CLONE: NATIVE FLP

ENTERED

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/086,542A

DATE: 08/09/2002

TIME: 15:49:58

Input Set : N:\Crf3\RULE60\10086542A.RAW

Output Set: N:\CRF4\08092002\J086542A.raw

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63      (ix) FEATURE:
64          (A) NAME/KEY: CDS
65          (B) LOCATION: 1..1269
68      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
70 ATG CCA CAA TTT GAT ATA TTA TGT AAA ACA CCA CCT AAG GTG CTT GTT      48
71 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val
72   1           5           10           15
74 CGT CAG TTT GTG GAA AGG TTT GAA AGA CCT TCA GGT GAG AAA ATA GCA      96
75 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala
76           20           25           30
78 TTA TGT GCT GCT GAA CTA ACC TAT TTA TGT TGG ATG ATT ACA CAT AAC      144
79 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn
80           35           40           45
82 GGA ACA GCA ATC AAG AGA GCC ACA TTC ATG AGC TAT AAT ACT ATC ATA      192
83 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile
84   50           55           60
86 AGC AAT TCG CTG AGT TTC GAT ATT GTC AAT AAA TCA CTC CAG TTT AAA      240
87 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys
88 65           70           75           80
90 TAC AAG ACG CAA AAA GCA ACA ATT CTG GAA GCC TCA TTA AAG AAA TTG      288
91 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu
92           85           90           95
94 ATT CCT GCT TGG GAA TTT ACA ATT ATT CCT TAC TAT GGA CAA AAA CAT      336
95 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His
96           100          105          110
98 CAA TCT GAT ATC ACT GAT ATT GTA AGT AGT TTG CAA TTA CAG TTC GAA      384
99 Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu
100          115          120          125
102 TCA TCG GAA GAA GCA GAT AAG GGA AAT AGC CAC AGT AAA AAA ATG CTT      432
103 Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu
104          130          135          140
106 AAA GCA CTT CTA AGT GAG GGT GAA AGC ATC TGG GAG ATC ACT GAG AAA      480
107 Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys
108 145          150          155          160
110 ATA CTA AAT TCG TTT GAG TAT ACT TCG AGA TTT ACA AAA ACA AAA ACT      528
111 Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr
112          165          170          175
114 TTA TAC CAA TTC CTC TTC CTA GCT ACT TTC ATC AAT TGT GGA AGA TTC      576
115 Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe
116          180          185          190
118 AGC GAT ATT AAG AAC GTT GAT CCG AAA TCA TTT AAA TTA GTC CAA AAT      624
119 Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn
120          195          200          205
122 AAG TAT CTG GGA GTA ATA ATC CAG TGT TTA GTG ACA GAG ACA AAG ACA      672
123 Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr
124          210          215          220
126 AGC GTT AGT AGG CAC ATA TAC TTC TTT AGC GCA AGG GGT AGG ATC GAT      720
127 Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
128 225          230          235          240

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130 CCA CTT GTA TAT TTG GAT GAA TTT TTG AGG AAT TCT GAA CCA GTC CTA      768
131 Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu
132          245          250          255
134 AAA CGA GTA AAT AGG ACC GGC AAT TCT TCA AGC AAT AAA CAG GAA TAC      816
135 Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr
136          260          265          270
138 CAA TTA TTA AAA GAT AAC TTA GTC AGA TCG TAC AAT AAA GCT TTG AAG      864
139 Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys
140          275          280          285
142 AAA AAT GCG CCT TAT TCA ATC TTT GCT ATA AAA AAT GGC CCA AAA TCT      912
143 Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser
144          290          295          300
146 CAC ATT GGA AGA CAT TTG ATG ACC TCA TTT CTT TCA ATG AAG GGC CTA      960
147 His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu
148 305          310          315          320
150 ACG GAG TTG ACT AAT GTT GTG GGA AAT TGG AGC GAT AAG CGT GCT TCT      1008
151 Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser
152          325          330          335
154 GCC GTG GCC AGG ACA ACG TAT ACT CAT CAG ATA ACA GCA ATA CCT GAT      1056
155 Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp
156          340          345          350
158 CAC TAC TTC GCA CTA GTT TCT CGG TAC TAT GCA TAT GAT CCA ATA TCA      1104
159 His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser
160          355          360          365
162 AAG GAA ATG ATA GCA TTG AAG GAT GAG ACT AAT CCA ATT GAG GAG TGG      1152
163 Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp
164          370          375          380
166 CAG CAT ATA GAA CAG CTA AAG GGT AGT GCT GAA GGA AGC ATA CGA TAC      1200
167 Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr
168 385          390          395          400
170 CCC GCA TGG ATT GGG ATA ATA TCA CAG GAG GTA CTA GAC TAC CTT TCA      1248
171 Pro Ala Trp Ile Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser
172          405          410          415
174 TCC TAC ATA AAT AGA CGC ATA TAAGTACGCA TTTAAGCATA AACACGCACT      1299
175 Ser Tyr Ile Asn Arg Arg Ile
176          420
178 ATCCCGTTCT TCTCATGTAT ATATATATAC AGGCAACACG CAGATATAGG TGCGACGTGA      1359
180 ACAGTGAGCT GTATGTGCGC A      1380
183 (2) INFORMATION FOR SEQ ID NO: 2:
185     (i) SEQUENCE CHARACTERISTICS:
186         (A) LENGTH: 423 amino acids
187         (B) TYPE: amino acid
188         (D) TOPOLOGY: linear
190     (ii) MOLECULE TYPE: protein
192     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
194 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val
195  1          5          10          15
197 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala
198          20          25          30

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200 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn
201          35                      40                      45
203 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile
204          50                      55                      60
206 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys
207 65          70                      75                      80
209 Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu
210          85                      90                      95
212 Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His
213          100                     105                     110
215 Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu
216          115                     120                     125
218 Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu
219          130                     135                     140
221 Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys
222 145          150                     155                     160
224 Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr
225          165                     170                     175
227 Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe
228          180                     185                     190
230 Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn
231          195                     200                     205
233 Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr
234          210                     215                     220
236 Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
237 225          230                     235                     240
239 Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu
240          245                     250                     255
242 Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr
243          260                     265                     270
245 Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys
246          275                     280                     285
248 Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser
249          290                     295                     300
251 His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu
252 305          310                     315                     320
254 Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser
255          325                     330                     335
257 Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp
258          340                     345                     350
260 His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser
261          355                     360                     365
263 Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp
264          370                     375                     380
266 Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr
267 385          390                     395                     400
269 Pro Ala Trp Ile Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser
270          405                     410                     415
272 Ser Tyr Ile Asn Arg Arg Ile

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273          420
275 (2) INFORMATION FOR SEQ ID NO: 3:
277   (i) SEQUENCE CHARACTERISTICS:
278       (A) LENGTH: 34 base pairs
279       (B) TYPE: nucleic acid
280       (C) STRANDEDNESS: single
281       (D) TOPOLOGY: linear
283   (ii) MOLECULE TYPE: DNA (genomic)
287   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
289 GAAGTTCCTA TTCTCTAGAA AGTATAGGAA CTTC          34
291 (2) INFORMATION FOR SEQ ID NO: 4:
293   (i) SEQUENCE CHARACTERISTICS:
294       (A) LENGTH: 68 base pairs
295       (B) TYPE: nucleic acid
296       (C) STRANDEDNESS: single
297       (D) TOPOLOGY: linear
299   (ii) MOLECULE TYPE: DNA (genomic)
303   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
305 GATCCCGGGC TACCATGGAG AAGTTCCTAT TCCGAAGTTC CTATTCTCTA GAAAGTATAG      60
307 GAACTTCA                                     68
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## VERIFICATION SUMMARY

DATE: 08/09/2002

PATENT APPLICATION: US/10/086,542A

TIME: 15:49:59

Input Set : N:\Crf3\RULE60\10086542A.RAW

Output Set: N:\CRF4\08092002\J086542A.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]